

The molecular basis of phenotypic adaptive changes in the common sole (*Solea solea*): disentangling fisheries from climate-induced evolution

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Recent studies have strongly indicated fishery-induced evolution of important life-history traits, such as age and size at maturation, growth, or reproductive effort in exploited fish populations. Most evidence is based on the analysis of phenotypic data, showing changes in maturation reaction norms, which for many species and populations have changed markedly over historical times corresponding to the intensity of fishing. However, the molecular basis of fishery-induced evolution has not been proved yet and requires further attention. We studied the neutral and adaptive genetic changes potentially induced by fisheries through the retrospective analysis of DNA from historical otolith collections from the North Sea sole population, which has been subjected to heavy harvesting for over 60 years. We evaluated the evolutionary trajectories of candidate genes involved in the growth axis and the brain–pituitary–gonad axis. We quantified the selective effects of fisheries on adaptive genetic variation and compared this pattern with a relatively stable neutral genetic baseline. Finally, we assessed the agreement between fisheries selection gradient and the direction of molecular genetic changes observed in sole, while estimating the proportional importance of alternative drivers (such as temperature increase) for creating the observed life-history changes.

Keywords: adaptive variation, climate change, fishery-induced evolution, management, over-fishing, sole.

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